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The KS330Bam sequence is an internal portion of a 918 bp ORF with 55-56% nucleotide identity to the ORF26 and BDLF1 genes of HSVSA and EBV, respectively (SEQ ID NO:46 and 47, respectively). The EBV and HSVSA translated amino acid sequences for these ORFs demonstrate extensive homology with the amino acid sequence encoded by the KS-associated 918 bp ORF (Figure 6). In HSVSA, the VP23 protein is a late structural protein involved in capsid construction. Reverse transcriptase (RT)-PCR of mRNA from a KS lesion is positive for transcribed KS330Bam mRNA and that indicates that this ORF is transcribed in KS lesions. Additional evidence for homology between the KS agent and herpesviruses comes from a comparison of the genomic organization of other potential ORFs on the 9404 bp sequence (Figure 3A). The 5' terminus of the sequence is composed of nucleotides having 66-67% nucleotide identity and 68-71% amino acid identity to corresponding regions of the major capsid protein (MCP) ORFs for both EBV and HSVSA. This putative MCP ORF of the KS agent lies immediately 5' to the BDLF1/ORF26 homolog which is a conserved orientation among herpesvirus subfamilies for these two genes. At the 3' end of this sequence, the reading frame has strong amino acid and nucleotide homology to HSVSA ORF 27. Thus, KS-associated DNA sequences at four loci in two separate regions with homologies to gamma herpesviral genomes have been identified.

Please delete line 6 of page 112 and replace it with the following:

Experiment 9: Isolation of KSHV

Please delete line 8 of page 114 and replace it with the following: